

Atty. Dkt. No. 058333-0112

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Yang-Do CHOI et al.

Title: GENES FOR S-ADENOSYL L-
METHIONINE:JASMONIC ACID
CARBOXYL
METHYLTRANSFERASE AND A
METHOD FOR THE
DEVELOPMENT OF PATHOGEN-
AND STRESS-RESISTANT
PLANTS USING THE GENES

Appl. No.: Unassigned

Filing Date: February 8, 2002

Examiner: Unassigned

Art Unit: 1638

PRELIMINARY AMENDMENT

Commissioner for Patents
Box PCT
Washington, D.C. 20231

Sir:

Prior to examination of the above-identified application, Applicants respectfully request that the above-identified application be amended as follows:

In the Claims:

In accordance with 37 C.F.R. §1.21, please substitute for claims 3, 4, 9, and 10 the following rewritten version of the same claims, as amended. The changes are shown explicitly in the attached "Marked-up Version of Amended Claims."

3. (Amended) The cDNA gene according to claim 2, which encodes an amino acid sequence represented by Sequence ID No. 1.

4. (Amended) The cDNA gene JMT according to claim 3, which encodes an amino acid sequence represented by Sequence ID No. 2 (Accession No. KCTC 0794BP).

9. (Amended) The method according to claim 8, wherein the gene encoding jasmonic acid carboxyl methyltransferase is the cDNA gene encoding a jasmonic acid carboxyl methyltransferase JMT having an amino acid sequence represented by Sequence ID No. 3.

10. (Amended) The method according to claim 9, wherein the gene encoding jasmonic acid carboxyl methyltransferase is the cDNA gene encoding an amino acid sequence represented by Sequence ID No. 1.

REMARKS

Applicants respectfully request that the foregoing amendments be made prior to examination of the present application. The amendments are made to correct multiple dependencies and do not change the scope of the invention.

Respectfully submitted,

Date February 8, 2002

FOLEY & LARDNER
Customer Number: 22428



22428

PATENT TRADEMARK OFFICE

Telephone: (202) 672-5407

Facsimile: (202) 672-5399

By Jayme A. Huleath
for Stephen A. Bent
Attorney for Applicants
Registration No. 29,768
Reg. No. 34,485

MARKED UP VERSION OF AMENDED CLAIMS

3. (Amended) The cDNA gene according to claim 2, which [contains] encodes an amino acid sequence represented by Sequence ID No. 1.

4. (Amended) The cDNA gene JMT according to claim 3, which [contains] encodes an amino acid sequence represented by Sequence ID No. 2 (Accession No. KCTC 0794BP).

9. (Amended) The method according to claim 8, wherein the gene encoding jasmonic acid carboxyl methyltransferase is the [gene as defined in claim 2] cDNA gene encoding a jasmonic acid carboxyl methyltransferase JMT having an amino acid sequence represented by Sequence ID No. 3.

10. (Amended) The method according to claim 9, wherein the gene encoding jasmonic acid carboxyl methyltransferase is the [gene as defined in claim 3 or 4] cDNA gene encoding an amino acid sequence represented by Sequence ID No. 1.

Rec'd PCT/PTO

13 JUN 2002

Atty. Dkt. No. 058333-0112

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant: Choi, Yang-Do *et al.*
Title: GENES FOR S-ADENOSYL L-METHIONINE: JASMONIC
ACID CARBOXYL METHYLTRANSFERASE AND A
METHOD FOR THE DEVELOPMENT OF PATHOGEN-AND
STRESS-RESISTANT PLANTS USING THE GENES
Appl. No.: 10/049,187
Filing Date: June 13, 2002
Examiner: Unassigned
Art Unit: Unassigned

AMENDMENT IN RESPONSE TO NOTICE UNDER 37 CFR §§1.821-825

Commissioner for Patents
Washington, D.C. 20231

Sir:

In response to the Notice to Comply With Requirements Under 35 U.S.C. 371 In the United States Designated/Elected Office (DO/EO/US) mailed April 16, 2002, please amend the application as follows:

Please amend the application as follows:

In the Specification:

Please amend the specification as shown:

Please delete the paragraph on page 5, lines 29 to page 6, line 3 and replace it with the following paragraph:

Figure 2 shows the amino acid sequence of protein derived from cDNA gene of JMT enzyme cloned from *Arabidopsis thaliana* in comparison to the amino acid sequence of protein derived from *SAMT* as a gene for known salicylic acid methyltransferase (Accession No. AF133053; Ross *et al.*,

1999). In Figure 2, AtJMT denotes JMT enzyme of *Arabidopsis thaliana* and SAMT (SEQ ID NO: 6) denotes salicylic acid methyltransferase of *Clarkia breweri*.

Please delete the paragraph on page 6, lines 4 to 8 and replace it with the following paragraph:

Figure 3 (SEQ ID NOS 7-8) shows the structure of recombinant gene pGST-JMT for expression of *JMT* gene in the form of a fusion protein with glutathione *S*-transferase by inserting *JMT* gene into pGEX-2T as *E. coli* expression vector. In Figure 3, Ptac denotes tac promoter and the underline indicates the nucleotide and amino acid sequences of amino terminal of JMT constituting the fusion protein.

REMARKS

Applicants believe that the present application is now in condition for allowance. Favorable reconsideration of the application as amended is respectfully requested.

The Examiner is invited to contact the undersigned by telephone if it is felt that a telephone interview would advance the prosecution of the present application.

Respectfully submitted,

Date 13 June 2002

By

S. A. Bent

Foley & Lardner
Washington Harbour
3000 K Street, N.W. Suite 500
Washington, DC 20007-5143
Telephone:
Facsimile:

Stephen A. Bent
Attorney for Applicant
Reg. No. 29,768

Should additional fees be necessary in connection with the filing of this paper, or if a petition for extension of time is required for timely acceptance of same, the Commissioner is hereby authorized to charge Deposit Account No. 19-0741 for any such fees; and applicant(s) hereby petition for any needed extension of time.

**MARKED UP VERSION ATTACHED TO AMENDMENT IN
SERIAL NO. 10/049,187**

**Marked up version of the paragraph starting at page 5, line 29 to page 6, line 3
is below:**

Figure 2 shows the amino acid sequence of protein derived from cDNA gene of JMT enzyme cloned from *Arabidopsis thaliana* in comparison to the amino acid sequence of protein derived from *SAMT* as a gene for known salicylic acid methyltransferase (Accession No. AF133053; Ross *et al.*, 1999). In Figure 2, AtJMT denotes JMT enzyme of *Arabidopsis thaliana* and SAMT (SEQ ID NO: 6) denotes salicylic acid methyltransferase of *Clarkia breweri*.

Marked up version of the paragraph starting at page 6, lines 4 to 8 is below:

Figure 3 (SEQ ID NOS 7-8) shows the structure of recombinant gene pGST-JMT for expression of *JMT* gene in the form of a fusion protein with glutathione *S*-transferase by inserting *JMT* gene into pGEX-2T as *E. coli* expression vector. In Figure 3, Ptac denotes tac promoter and the underline indicates the nucleotide and amino acid sequences of amino terminal of JMT constituting the fusion protein.

SEQUENCE LISTING

<110> CHOI, YANG-DO
 CHEONG, JONG-JOO
 LEE, JONG-SEOB
 SONG, JONG-TAE
 SONG, SANG-IK
 SEO, HAK-SOO
 KOO, YEON-JONG

<120> GENES FOR S-ADENOSYL L-METHIONINE: JASMONIC ACID
 CARBOXYL METHYLTRANSFERASE AND A METHOD FOR THE
 DEVELOPMENT OF PATHOGEN- AND STRESS-RESISTANT PLANTS
 USING THE GENES

<130> 058333/0112

<140> 10/049,187

<141> 2002-02-08

<150> PCT/KR01/00953

<151> 2001-06-05

<160> 8

<170> PatentIn Ver. 2.1

<210> 1

<211> 1170

<212> DNA

<213> Arabidopsis thaliana

<400> 1

```

atggaggttaa tgcgagttct tcacatgaac aaaggaaacg gggaaacaag ttatgccaaag 60
aactccaccg ctcagagcaa cataatatct ctaggcagaa gagtaatgga cgaggccttg 120
aagaagttaa tgatgagcaa ttcagagatt tcgagcattg gaatcgccga cttaggctgc 180
tcctccggtc cgaacagtct cttgtccatc tccaacatag ttgacacgat ccacaacttg 240
tgtcctgacc tcgaccgtcc agtccctgag ctcagagtct ctctcaacga cctccctagc 300
aatgacttca actacatatg tgcttctttg ccagagtttt acgaccgggt taataataac 360
aaggagggtt tagggttcgg tcgtggagga ggagaatcgt gttttgtgtc ggccgtccca 420
ggttcgttct acggacgttt gtttcctcgc cggagccttc actttgtgca ttcttcttct 480
agtttacatt ggttgtctca ggttccatgt cgtgaggcgg agaaggaaga caggacaata 540
acagctgatt tagaaaacat ggggaaaata tacatatcaa agacaagtcc taagagtgca 600
cataaagctt atgctcttca attccaaact gatttcttgg tttttttgag gtcacgatct 660
gaggagtttg tcccgggagg ccgaatggtt ttatcgttcc ttggtagaag atcactggat 720
cccacaaccg aagagagttg ctatcaatgg gaactcctag ctcaagctct tatgtccatg 780
gccaaagagg gtatcatcga ggaagagaag atcgatgctt tcaacgctcc ttactatgct 840
gcgagctccg aagagttgaa aatggtgata gagaaagaag ggtcattttc gatcgatagg 900
cttgagataa gtccgattga ttgggaaggt gggagtatca gtgaggagag ttatgacctt 960
gcaataaggt ccaaaccgga agccctagct agtggccgaa gagtgtctaa taccataaga 1020
gctgtggctg agccgatgct agaacctact ttcggtgaaa atgtgatgga cgagcttttt 1080
gaaaggatat caaagatcgt gggagagtac ttctatgtaa gctcgccacg atacgctatt 1140
gttattcttt cgctcgttag aaccggttga                               1170

```

<210> 2

<211> 1476

3

2

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (15)..(1181)

<223> open reading frame for JMT

<400> 2

```

aaagagagag agag atg gag gta atg cga gtt ctt cac atg aac aaa gga 50
      Met Glu Val Met Arg Val Leu His Met Asn Lys Gly
        1              5              10

aac ggg gaa aca agt tat gcc aag aac tcc acc gct cag agc aac ata 98
Asn Gly Glu Thr Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn Ile
      15              20              25

ata tct cta ggc aga aga gta atg gac gag gcc ttg aag aag tta atg 146
Ile Ser Leu Gly Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met
      30              35              40

atg agc aat tca gag att tcg agc att gga atc gcc gac tta ggc tgc 194
Met Ser Asn Ser Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys
      45              50              55              60

tcc tcc ggt ccg aac agt ctc ttg tcc atc tcc aac ata gtt gac acg 242
Ser Ser Gly Pro Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr
      65              70              75

atc cac aac ttg tgt cct gac ctc gac cgt cca gtc cct gag ctc aga 290
Ile His Asn Leu Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg
      80              85              90

gtc tct ctc aac gac ctc cct agc aat gac ttc aac tac ata tgt gct 338
Val Ser Leu Asn Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala
      95              100              105

tct ttg cca gag ttt tac gac cgg gtt aat aat aac aag gag ggt tta 386
Ser Leu Pro Glu Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu
      110              115              120

ggg ttc ggt cgt gga gga gga gaa tcg tgt ttt gtg tcg gcc gtc cca 434
Gly Phe Gly Arg Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro
      125              130              135              140

ggt tcg ttc tac gga cgt ttg ttt cct cgc cgg agc ctt cac ttt gtg 482
Gly Ser Phe Tyr Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val
      145              150              155

cat tct tct tct agt tta cat tgg ttg tct cag gtt cca tgt cgt gag 530
His Ser Ser Ser Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu
      160              165              170

gcg gag aag gaa gac agg aca ata aca gct gat tta gaa aac atg ggg 578
Ala Glu Lys Glu Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly
      175              180              185

```


aaa ata tac ata tca aag aca agt cct aag agt gca cat aaa gct tat 626
 Lys Ile Tyr Ile Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr
 190 195 200

gct ctt caa ttc caa act gat ttc ttg gtt ttt ttg agg tca cga tct 674
 Ala Leu Gln Phe Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser
 205 210 215 220

gag gag ttg gtc ccg gga ggc cga atg gtt tta tcg ttc ctt ggt aga 722
 Glu Glu Leu Val Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg
 225 230 235

aga tca ctg gat ccc aca acc gaa gag agt tgc tat caa tgg gaa ctc 770
 Arg Ser Leu Asp Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu
 240 245 250

cta gct caa gct ctt atg tcc atg gcc aaa gag ggt atc atc gag gaa 818
 Leu Ala Gln Ala Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu
 255 260 265

gag aag atc gat gct ttc aac gct cct tac tat gct gcg agc tcc gaa 866
 Glu Lys Ile Asp Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu
 270 275 280

gag ttg aaa atg gtg ata gag aaa gaa ggg tca ttt tcg atc gat agg 914
 Glu Leu Lys Met Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg
 285 290 295 300

ctt gag ata agt ccg att gat tgg gaa ggt ggg agt atc agt gag gag 962
 Leu Glu Ile Ser Pro Ile Asp Trp Glu Gly Gly Ser Ile Ser Glu Glu
 305 310 315

agt tat gac ctt gca ata agg tcc aaa ccc gaa gcc cta gct agt ggc 1010
 Ser Tyr Asp Leu Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly
 320 325 330

cga aga gtg tct aat acc ata aga gct gtg gtc gag ccg atg cta gaa 1058
 Arg Arg Val Ser Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu
 335 340 345

cct act ttc ggt gaa aat gtg atg gac gag ctt ttt gaa agg tat gca 1106
 Pro Thr Phe Gly Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala
 350 355 360

aag atc gtg gga gag tac ttc tat gta agc tcg cca cga tac gct att 1154
 Lys Ile Val Gly Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile
 365 370 375 380

gtt att ctt tcg ctc gtt aga acc ggt tgatcgtgtt ataacatatg 1201
 Val Ile Leu Ser Leu Val Arg Thr Gly
 385

ccaatataca tgtctttggg cctacaatga catgatttgg tagttttcta atcaagcata 1261

tgtaatataa tttgcttcga gaataaaata ataaaataaa gtgtgatgtt acggtagacc 1321

cttttttttt tttcttcatt tacggtagac ctatagtatt aaaacaaata gaatcagctg 1381

gttcggacct tgaaatgaga gagcttggat gcatgtagac gcattagtcg tgaattattc 1441

aaatagaact accttttggg ccaaaaaaaaa aaaaa 1476

<210> 3

<211> 389

<212> PRT

<213> Arabidopsis thaliana

<400> 3

Met Glu Val Met Arg Val Leu His Met Asn Lys Gly Asn Gly Glu Thr
1 5 10 15

Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn Ile Ile Ser Leu Gly
20 25 30

Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met Met Ser Asn Ser
35 40 45

Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
50 55 60

Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr Ile His Asn Leu
65 70 75 80

Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg Val Ser Leu Asn
85 90 95

Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala Ser Leu Pro Glu
100 105 110

Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu Gly Phe Gly Arg
115 120 125

Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro Gly Ser Phe Tyr
130 135 140

Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val His Ser Ser Ser
145 150 155 160

Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu Ala Glu Lys Glu
165 170 175

Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly Lys Ile Tyr Ile
180 185 190

Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr Ala Leu Gln Phe
195 200 205

Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser Glu Glu Leu Val
210 215 220

Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg Arg Ser Leu Asp
225 230 235 240

Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu Leu Ala Gln Ala
245 250 255

Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu Glu Lys Ile Asp
 260 265 270
 Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu Glu Leu Lys Met
 275 280 285
 Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg Leu Glu Ile Ser
 290 295 300
 Pro Ile Asp Trp Glu Gly Gly Ser Ile Ser Glu Glu Ser Tyr Asp Leu
 305 310 315 320
 Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly Arg Arg Val Ser
 325 330 335
 Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu Pro Thr Phe Gly
 340 345 350
 Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala Lys Ile Val Gly
 355 360 365
 Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile Val Ile Leu Ser
 370 375 380
 Leu Val Arg Thr Gly
 385

<210> 4

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 5' primer for
PCR of JMT gene

<400> 4

cgcgtccgaa ttcgagagag agagaatgga

30

<210> 5

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 3' primer for
PCR of JMT gene

<400> 5

tttgaagaat tcacgactaa tgcgtctaca

30

<210> 6

<211> 359

<212> PRT

<213> Clarkia breweri

<400> 6

Met Asp Val Arg Gln Val Leu His Met Lys Gly Gly Ala Gly Glu Asn
 1 5 10 15

Ser Tyr Ala Met Asn Ser Phe Ile Gln Arg Gln Val Ile Ser Ile Thr
 20 25 30

Lys Pro Ile Thr Glu Ala Ala Ile Thr Ala Leu Tyr Ser Gly Asp Thr
 35 40 45

Val Thr Thr Arg Leu Ala Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
 50 55 60

Asn Ala Leu Phe Ala Val Thr Glu Leu Ile Lys Thr Val Glu Glu Leu
 65 70 75 80

Arg Lys Lys Met Gly Arg Glu Asn Ser Pro Glu Tyr Gln Ile Phe Leu
 85 90 95

Asn Asp Leu Pro Gly Asn Asp Phe Asn Ala Ile Phe Arg Ser Leu Pro
 100 105 110

Ile Glu Asn Asp Val Asp Gly Val Cys Phe Ile Asn Gly Val Pro Gly
 115 120 125

Ser Phe Tyr Gly Arg Leu Phe Pro Arg Asn Thr Leu His Phe Ile His
 130 135 140

Ser Ser Tyr Ser Leu Met Trp Leu Ser Gln Val Pro Ile Gly Ile Glu
 145 150 155 160

Ser Asn Lys Gly Asn Ile Tyr Met Ala Asn Thr Cys Pro Gln Ser Val
 165 170 175

Leu Asn Ala Tyr Tyr Lys Gln Phe Gln Glu Asp His Ala Leu Phe Leu
 180 185 190

Arg Cys Arg Ala Gln Glu Val Val Pro Gly Gly Arg Met Val Leu Thr
 195 200 205

Ile Leu Gly Arg Arg Ser Glu Asp Arg Ala Ser Thr Glu Cys Cys Leu
 210 215 220

Ile Trp Gln Leu Leu Ala Met Ala Leu Asn Gln Met Val Ser Glu Gly
 225 230 235 240

Leu Ile Glu Glu Glu Lys Met Asp Lys Phe Asn Ile Pro Gln Tyr Thr
 245 250 255

Pro Ser Pro Thr Glu Val Glu Ala Glu Ile Leu Lys Glu Gly Ser Phe
 260 265 270

Leu Ile Asp His Ile Glu Ala Ser Glu Ile Tyr Trp Ser Ser Cys Thr
 275 280 285

Lys Asp Gly Asp Gly Gly Gly Ser Val Glu Glu Glu Gly Tyr Asn Val
 290 295 300

Ala Arg Cys Met Arg Ala Val Ala Glu Pro Leu Leu Leu Asp His Phe
 305 310 315 320

Gly Glu Ala Ile Ile Glu Asp Val Phe His Arg Tyr Lys Leu Leu Ile
 325 330 335

Ile Glu Arg Met Ser Lys Glu Lys Thr Lys Phe Ile Asn Val Ile Val
 340 345 350

Ser Leu Ile Arg Lys Ser Asp
 355

<210> 7
 <211> 48
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 nucleotide sequence

<220>
 <221> CDS
 <222> (1)..(48)

<400> 7
 ctg gtt ccg cgt gga tcc ccg gga att cga caa aga gag aga gag atg 48
 Leu Val Pro Arg Gly Ser Pro Gly Ile Arg Gln Arg Glu Arg Glu Met
 1 5 10 15

<210> 8
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 peptide

<400> 8
 Leu Val Pro Arg Gly Ser Pro Gly Ile Arg Gln Arg Glu Arg Glu Met
 1 5 10 15

10049187.05.15.02



PCT

ENTERED

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/049,187

DATE: 07/15/2002

TIME: 12:38:09

Input Set : A:\58333112.app

Output Set: N:\CRF3\07152002\J049187.raw

```

3 <110> APPLICANT: CHOI, YANG-DO
4     CHEONG, JONG-JOO
5     LEE, JONG-SEOB
6     SONG, JONG-TAE
7     SONG, SANG-IK
8     SEO, HAK-SOO
9     KOO, YEON-JONG
11 <120> TITLE OF INVENTION: GENES FOR S-ADENOSYL L-METHIONINE: JASMONIC ACID
12     CARBOXYL METHYLTRANSFERASE AND A METHOD FOR THE
13     DEVELOPMENT OF PATHOGEN- AND STRESS-RESISTANT PLANTS
14     USING THE GENES
16 <130> FILE REFERENCE: 058333/0112
18 <140> CURRENT APPLICATION NUMBER: 10/049,187
C--> 19 <141> CURRENT FILING DATE: 2002-06-13
21 <150> PRIOR APPLICATION NUMBER: PCT/KR01/00953
22 <151> PRIOR FILING DATE: 2001-06-05
24 <160> NUMBER OF SEQ ID NOS: 8
26 <170> SOFTWARE: PatentIn Ver. 2.1
28 <210> SEQ ID NO: 1
29 <211> LENGTH: 1170
30 <212> TYPE: DNA
31 <213> ORGANISM: Arabidopsis thaliana
33 <400> SEQUENCE: 1
34 atggaggttaa tgcgagttct tcacatgaac aaaggaaacg gggaaacaag ttatgccaa 60
35 aactccaccg ctcagagcaa cataatatct ctaggcagaa gagtaatgga cgaggccttg 120
36 aagaagttaa tgatgagcaa ttcagagatt tcgagcattg gaatcgccga cttaggctgc 180
37 tcctccggtc cgaacagtct cttgtccatc tccaacatag ttgacacgat ccacaacttg 240
38 tgtcctgacc tcgaccgtcc agtccctgag ctcagagtct ctctcaacga cctccctagc 300
39 aatgacttca actacatatg tgcttctttg ccagagtttt acgaccgggt taataataac 360
40 aaggagggtt tagggttcg tegtggagga ggagaatcgt gttttgtgtc ggccgtccca 420
41 ggttcgttct acggacgttt gtttcctcgc cggagccttc actttgtgca ttcttcttct 480
42 agtttacatt ggttgtctca ggttccatgt cgtgaggcgg agaaggaaga caggacaata 540
43 acagctgatt tagaaaacat ggggaaaata tacatatcaa agacaagtcc taagagtgca 600
44 cataaagctt atgctcttca attccaaaact gatttcttgg tttttttgag gtcacgatct 660
45 gaggagttag tcccgggagg ccgaatggtt ttatcgttcc ttggtagaag atcactggat 720
46 cccacaaccg aagagagttg ctatcaatgg gaactcctag ctcaagctct tatgtccatg 780
47 gccaaagagg gtatcatcga ggaagagaa atcgatgctt tcaacgctcc ttactatgct 840
48 gcgagctccg aagagttgaa aatggtgata gagaaagaag ggtcattttc gatcgatagg 900
49 cttgagataa gtccgattga ttgggaaggt gggagtatca gtgaggagag ttatgacctt 960
50 gcaataaggt ccaaaccgga agccctagct agtgccgaa gagtgtctaa taccataaga 1020
51 gctgtggtcg agccgatgct agaacctact ttcggtgaaa atgtgatgga cgagcttttt 1080
52 gaaaggtatg caaagatcgt gggagagtac ttctatgtaa gctcgccacg atacgctatt 1140
53 gttattcttt cgctcgttag aaccggttga 1170

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/049,187

DATE: 07/15/2002

TIME: 12:38:09

Input Set : A:\58333112.app

Output Set: N:\CRF3\07152002\J049187.raw

```

56 <210> SEQ ID NO: 2
57 <211> LENGTH: 1476
58 <212> TYPE: DNA
59 <213> ORGANISM: Arabidopsis thaliana
61 <220> FEATURE:
62 <221> NAME/KEY: CDS
63 <222> LOCATION: (15)..(1181)
64 <223> OTHER INFORMATION: open reading frame for JMT
66 <400> SEQUENCE: 2
67 aaagagagag agag atg gag gta atg cga gtt ctt cac atg aac aaa gga 50
68 Met Glu Val Met Arg Val Leu His Met Asn Lys Gly
69 1 5 10
71 aac ggg gaa aca agt tat gcc aag aac tcc acc gct cag agc aac ata 98
72 Asn Gly Glu Thr Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn Ile
73 15 20 25
75 ata tct cta ggc aga aga gta atg gac gag gcc ttg aag aag tta atg 146
76 Ile Ser Leu Gly Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met
77 30 35 40
79 atg agc aat tca gag att tcg agc att gga atc gcc gac tta ggc tgc 194
80 Met Ser Asn Ser Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys
81 45 50 55 60
83 tcc tcc ggt ccg aac agt ctc ttg tcc atc tcc aac ata gtt gac acg 242
84 Ser Ser Gly Pro Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr
85 65 70 75
87 atc cac aac ttg tgt cct gac ctc gac cgt cca gtc cct gag ctc aga 290
88 Ile His Asn Leu Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg
89 80 85 90
91 gtc tct ctc aac gac ctc cct agc aat gac ttc aac tac ata tgt gct 338
92 Val Ser Leu Asn Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala
93 95 100 105
95 tct ttg cca gag ttt tac gac cgg gtt aat aat aac aag gag ggt tta 386
96 Ser Leu Pro Glu Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu
97 110 115 120
99 ggg ttc ggt cgt gga gga gga gaa tcg tgt ttt gtg tcg gcc gtc cca 434
100 Gly Phe Gly Arg Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro
101 125 130 135 140
103 ggt tcg ttc tac gga cgt ttg ttt cct cgc cgg agc ctt cac ttt gtg 482
104 Gly Ser Phe Tyr Gly Arg Leu Phe Pro Arg Arg Ser Leu His Phe Val
105 145 150 155
107 cat tct tct tct agt tta cat tgg ttg tct cag gtt cca tgt cgt gag 530
108 His Ser Ser Ser Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu
109 160 165 170
111 gcg gag aag gaa gac agg aca ata aca gct gat tta gaa aac atg ggg 578
112 Ala Glu Lys Glu Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly
113 175 180 185
115 aaa ata tac ata tca aag aca agt cct aag agt gca cat aaa gct tat 626
116 Lys Ile Tyr Ile Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr
117 190 195 200
119 gct ctt caa ttc caa act gat ttc ttg gtt ttt ttg agg tca cga tct 674

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/049,187

DATE: 07/15/2002

TIME: 12:38:09

Input Set : A:\58333112.app

Output Set: N:\CRF3\07152002\J049187.raw

```

120 Ala Leu Gln Phe Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser
121 205 210 215 220
123 gag gag ttg gtc ccg gga ggc cga atg gtt tta tcg ttc ctt ggt aga 722
124 Glu Glu Leu Val Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg
125 225 230 235
127 aga tca ctg gat ccc aca acc gaa gag agt tgc tat caa tgg gaa ctc 770
128 Arg Ser Leu Asp Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu
129 240 245 250
131 cta gct caa gct ctt atg tcc atg gcc aaa gag ggt atc atc gag gaa 818
132 Leu Ala Gln Ala Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu
133 255 260 265
135 gag aag atc gat gct ttc aac gct cct tac tat gct gcg agc tcc gaa 866
136 Glu Lys Ile Asp Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu
137 270 275 280
139 gag ttg aaa atg gtg ata gag aaa gaa ggg tca ttt tcg atc gat agg 914
140 Glu Leu Lys Met Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg
141 285 290 295 300
143 ctt gag ata agt ccg att gat tgg gaa ggt ggg agt atc agt gag gag 962
144 Leu Glu Ile Ser Pro Ile Asp Trp Glu Gly Gly Ser Ile Ser Glu Glu
145 305 310 315
147 agt tat gac ctt gca ata agg tcc aaa ccc gaa gcc cta gct agt ggc 1010
148 Ser Tyr Asp Leu Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly
149 320 325 330
151 cga aga gtg tct aat acc ata aga gct gtg gtc gag ccg atg cta gaa 1058
152 Arg Arg Val Ser Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu
153 335 340 345
155 cct act ttc ggt gaa aat gtg atg gac gag ctt ttt gaa agg tat gca 1106
156 Pro Thr Phe Gly Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala
157 350 355 360
159 aag atc gtg gga gag tac ttc tat gta agc tcg cca cga tac gct att 1154
160 Lys Ile Val Gly Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile
161 365 370 375 380
163 gtt att ctt tcg ctc gtt aga acc ggt tgatcgtggtt ataacatatg 1201
164 Val Ile Leu Ser Leu Val Arg Thr Gly
165 385
167 ccaatataca tgtctttggg cctacaatga catgatttgg tagttttcta atcaagcata 1261
169 tgtaatatataa tttgcttcga gaataaaata ataaaataaaa gtgtgatggtt acggtagacc 1321
171 cttttttttt tttcttcatt tacggtagac ctatagtatt aaaacaaata gaatcagctg 1381
173 gttcggacct tgaaatgaga gagcttggat gcatgtagac gcattagtcg tgaattattc 1441
175 aaatagaact accttttggg ccaaaaaaaaa aaaaa 1476
178 <210> SEQ ID NO: 3
179 <211> LENGTH: 389
180 <212> TYPE: PRT
181 <213> ORGANISM: Arabidopsis thaliana
183 <400> SEQUENCE: 3
184 Met Glu Val Met Arg Val Leu His Met Asn Lys Gly Asn Gly Glu Thr
185 1 5 10 15
187 Ser Tyr Ala Lys Asn Ser Thr Ala Gln Ser Asn Ile Ile Ser Leu Gly
188 20 25 30

```


RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/049,187

DATE: 07/15/2002

TIME: 12:38:09

Input Set : A:\58333112.app

Output Set: N:\CRF3\07152002\J049187.raw

```

190 Arg Arg Val Met Asp Glu Ala Leu Lys Lys Leu Met Met Ser Asn Ser
191          35                      40                      45
193 Glu Ile Ser Ser Ile Gly Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
194          50                      55                      60
196 Asn Ser Leu Leu Ser Ile Ser Asn Ile Val Asp Thr Ile His Asn Leu
197 65          70                      75                      80
199 Cys Pro Asp Leu Asp Arg Pro Val Pro Glu Leu Arg Val Ser Leu Asn
200          85                      90                      95
202 Asp Leu Pro Ser Asn Asp Phe Asn Tyr Ile Cys Ala Ser Leu Pro Glu
203          100                     105                     110
205 Phe Tyr Asp Arg Val Asn Asn Asn Lys Glu Gly Leu Gly Phe Gly Arg
206          115                     120                     125
208 Gly Gly Gly Glu Ser Cys Phe Val Ser Ala Val Pro Gly Ser Phe Tyr
209          130                     135                     140
211 Gly Arg Leu Phe Pro Arg Ser Leu His Phe Val His Ser Ser Ser
212 145          150                     155                     160
214 Ser Leu His Trp Leu Ser Gln Val Pro Cys Arg Glu Ala Glu Lys Glu
215          165                     170                     175
217 Asp Arg Thr Ile Thr Ala Asp Leu Glu Asn Met Gly Lys Ile Tyr Ile
218          180                     185                     190
220 Ser Lys Thr Ser Pro Lys Ser Ala His Lys Ala Tyr Ala Leu Gln Phe
221          195                     200                     205
223 Gln Thr Asp Phe Leu Val Phe Leu Arg Ser Arg Ser Glu Glu Leu Val
224          210                     215                     220
226 Pro Gly Gly Arg Met Val Leu Ser Phe Leu Gly Arg Arg Ser Leu Asp
227 225          230                     235                     240
229 Pro Thr Thr Glu Glu Ser Cys Tyr Gln Trp Glu Leu Leu Ala Gln Ala
230          245                     250                     255
232 Leu Met Ser Met Ala Lys Glu Gly Ile Ile Glu Glu Glu Lys Ile Asp
233          260                     265                     270
235 Ala Phe Asn Ala Pro Tyr Tyr Ala Ala Ser Ser Glu Glu Leu Lys Met
236          275                     280                     285
238 Val Ile Glu Lys Glu Gly Ser Phe Ser Ile Asp Arg Leu Glu Ile Ser
239          290                     295                     300
241 Pro Ile Asp Trp Glu Gly Gly Ser Ile Ser Glu Glu Ser Tyr Asp Leu
242 305          310                     315                     320
244 Ala Ile Arg Ser Lys Pro Glu Ala Leu Ala Ser Gly Arg Arg Val Ser
245          325                     330                     335
247 Asn Thr Ile Arg Ala Val Val Glu Pro Met Leu Glu Pro Thr Phe Gly
248          340                     345                     350
250 Glu Asn Val Met Asp Glu Leu Phe Glu Arg Tyr Ala Lys Ile Val Gly
251          355                     360                     365
253 Glu Tyr Phe Tyr Val Ser Ser Pro Arg Tyr Ala Ile Val Ile Leu Ser
254          370                     375                     380
256 Leu Val Arg Thr Gly
257 385
260 <210> SEQ ID NO: 4
261 <211> LENGTH: 30
262 <212> TYPE: DNA

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/049,187

DATE: 07/15/2002

TIME: 12:38:09

Input Set : A:\58333112.app

Output Set: N:\CRF3\07152002\J049187.raw

```

263 <213> ORGANISM: Artificial Sequence
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Description of Artificial Sequence: 5' primer for
267     PCR of JMT gene
269 <400> SEQUENCE: 4
270 cgcgtccgaa ttcgagagag agagaatgga
273 <210> SEQ ID NO: 5
274 <211> LENGTH: 30
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Description of Artificial Sequence: 3' primer for
280     PCR of JMT gene
282 <400> SEQUENCE: 5
283 tttgaagaat tcacgactaa tgcgtctaca
286 <210> SEQ ID NO: 6
287 <211> LENGTH: 359
288 <212> TYPE: PRT
289 <213> ORGANISM: Clarkia breweri
291 <400> SEQUENCE: 6
292 Met Asp Val Arg Gln Val Leu His Met Lys Gly Gly Ala Gly Glu Asn
293   1          5          10          15
295 Ser Tyr Ala Met Asn Ser Phe Ile Gln Arg Gln Val Ile Ser Ile Thr
296          20          25          30
298 Lys Pro Ile Thr Glu Ala Ala Ile Thr Ala Leu Tyr Ser Gly Asp Thr
299          35          40          45
301 Val Thr Thr Arg Leu Ala Ile Ala Asp Leu Gly Cys Ser Ser Gly Pro
302          50          55          60
304 Asn Ala Leu Phe Ala Val Thr Glu Leu Ile Lys Thr Val Glu Glu Leu
305   65          70          75          80
307 Arg Lys Lys Met Gly Arg Glu Asn Ser Pro Glu Tyr Gln Ile Phe Leu
308          85          90          95
310 Asn Asp Leu Pro Gly Asn Asp Phe Asn Ala Ile Phe Arg Ser Leu Pro
311          100         105         110
313 Ile Glu Asn Asp Val Asp Gly Val Cys Phe Ile Asn Gly Val Pro Gly
314          115         120         125
316 Ser Phe Tyr Gly Arg Leu Phe Pro Arg Asn Thr Leu His Phe Ile His
317          130         135         140
319 Ser Ser Tyr Ser Leu Met Trp Leu Ser Gln Val Pro Ile Gly Ile Glu
320 145          150         155         160
322 Ser Asn Lys Gly Asn Ile Tyr Met Ala Asn Thr Cys Pro Gln Ser Val
323          165         170         175
325 Leu Asn Ala Tyr Tyr Lys Gln Phe Gln Glu Asp His Ala Leu Phe Leu
326          180         185         190
328 Arg Cys Arg Ala Gln Glu Val Val Pro Gly Gly Arg Met Val Leu Thr
329          195         200         205
331 Ile Leu Gly Arg Arg Ser Glu Asp Arg Ala Ser Thr Glu Cys Cys Leu
332          210         215         220
334 Ile Trp Gln Leu Leu Ala Met Ala Leu Asn Gln Met Val Ser Glu Gly

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/049,187

DATE: 07/15/2002

TIME: 12:38:10

Input Set : A:\58333112.app

Output Set: N:\CRF3\07152002\J049187.raw

L:19 M:271 C: Current Filing Date differs, Replaced Current Filing Date